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Sim

Click [here](#) to view these alignments graphically with the [LALNVIEW](#) program (mime-type *chemical/x-aln2*).

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Results of SIM with:

Sequence 1: SEQ (434 residues)
Sequence 2: [P10845](#), (1296 residues)

using the parameters:

Comparison matrix: BLOSUM62
Number of alignments computed: 5
Gap open penalty: 12
Gap extension penalty: 4



Evaluate the significance of this protein sequence similarity score using [PRSS](#) at [EMBnet-CH](#).

99.8% identity in 434 residues overlap; Score: 2296.0; Gap frequency: 0.0%

```

SEQ          1 MSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESS
P10845,      863 LSTFTEYIKNIINTSILNLRYESNHLIDLSRYASKINIGSKVNFDPIDKNQIQLFNLESS
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SEQ          61 KIEVILKNAIVNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGE
P10845,      923 KIEVILKNAIVNSMYENFSTSFWIRIPKYFNSISLNNEYTIINCMENNSGWKVS LNYGE
                *****

SEQ          121 IIWTLQDTQEIKQRVVF KYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPIS
P10845,      983 IIWTLQDTQEIKQRVVF KYSQMINISDYINRWIFVTITNNRLNNSKIYINGRLIDQKPIS
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SEQ          181 NLGNIHASNNIMFKLDGCRDTHRYIWI KYFNLFDKELNEKEIKDLYDNQSN SGILKDFWG
P10845,     1043 NLGNIHASNNIMFKLDGCRDTHRYIWI KYFNLFDKELNEKEIKDLYDNQSN SGILKDFWG
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SEQ          241 DY LQYDKPY YMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFII
P10845,     1103 DY LQYDKPY YMLNLYDPNKYVDVNNVGIRGYMYLKGPRGSVMTTNIYLNSSLYRGTKFII
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SEQ 301 KKYASGNKDNIVRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVV
P10845, 1163 KKYASGNKDNIVRNNDRVYINVVVKNEYRLATNASQAGVEKILSALEIPDVGNLSQVVV

SEQ 361 MKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGCWS
P10845, 1223 MKSKNDQGITNKCKMNLQDNNGNDIGFIGFHQFNNAKLVASNWNRYQIERSSRTLGCWS

SEQ 421 EFIPVDDGWGERPL
P10845, 1283 EFIPVDDGWGERPE

34.8% identity in 23 residues overlap; Score: 41.0; Gap frequency: 0.0%

SEQ 207 IKYFNLFDKELNEKEIKDLYDNQ
P10845, 805 VKRLEDFDASLKDALLKYIIDNR
* ** *

29.4% identity in 34 residues overlap; Score: 39.0; Gap frequency: 0.0%

SEQ 27 IDLSRYASKINIGSKVNFDPIDKNQIQLFNLESS
P10845, 367 LNFDAVFKINIVPKVNYTIYDGFNLRNTNLAAN
**** ** *




25.0% identity in 28 residues overlap; Score: 39.0; Gap frequency: 0.0%

SEQ 242 YLQYDKPYMYMLNLYDPNKYVDVNNVGIR
P10845, 366 YLNFDAVFKINIVPKVNYTIYDGFNLR
** ** *

31.8% identity in 22 residues overlap; Score: 37.0; Gap frequency: 0.0%

SEQ 344 LSALEIPDVGNLSQVVVMKSKN
P10845, 19 IAYIKIPNVGQMOPVKAFKIHN
** ** *

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☐

Range: from to
 Features:
 ☐ SNP
 ☐ CDD
 ☒ MGC
 ☐ HPRD
 ☐ STS

☐ 1: [P10845](#). Reports Botulinum neuroto...[gi:399133]

[BLink](#), [Links](#)

LOCUS P10845 1296 aa linear BCT 01-MAY-2005
 DEFINITION Botulinum neurotoxin type A precursor (BoNT/A) (Bontoxilysin A) (BOTOX) [Contains: Botulinum neurotoxin A light-chain; Botulinum neurotoxin A heavy-chain].
 ACCESSION P10845
 VERSION P10845 GI:399133
 DBSOURCE swissprot: locus BXA1_CLOBO, accession [P10845](#); class: standard.
 extra accessions: P01561, P18639, created: Jul 1, 1989.
 sequence updated: Jul 1, 1993.
 annotation updated: May 1, 2005.
 xrefs: [X52066.1](#), [CAA36289.1](#), [M30196.1](#), [AAA23262.1](#), [X92973.1](#), [CAA63551.1](#), [D67030.1](#), [BAA11051.1](#), [M27892.1](#), [AAA23269.1](#), [BTCLAB](#), [3BTAA](#)
 xrefs (non-sequence databases): MEROPSM27.002, InterProIPR008985, InterProIPR011065, InterProIPR006025, InterProIPR000395, PfamPF01742, PRINTSPR00760, ProDomPD001963, PROSITEPS00142
 KEYWORDS 3D-structure; Direct protein sequencing; Hydrolase; Metalloprotease; Neurotoxin; Pharmaceutical; Protease; Toxin; Transmembrane; Zinc.
 SOURCE Clostridium botulinum
 ORGANISM [Clostridium botulinum](#)
 Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
 REFERENCE 1 (residues 1 to 1296)
 AUTHORS Thompson,D.E., Brehm,J.K., Oultram,J.D., Swinfield,T.J., Shone,C.C., Atkinson,T., Melling,J. and Minton,N.P.
 TITLE The complete amino acid sequence of the Clostridium botulinum type A neurotoxin, deduced by nucleotide sequence analysis of the encoding gene
 JOURNAL Eur. J. Biochem. 189 (1), 73-81 (1990)
 PUBMED [2185020](#)
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=Type A / NCTC 2916
 REFERENCE 2 (residues 1 to 1296)
 AUTHORS Binz,T., Kurazono,H., Wille,M., Frevert,J., Wernars,K. and Niemann,H.
 TITLE The complete sequence of botulinum neurotoxin type A and comparison with other clostridial neurotoxins
 JOURNAL J. Biol. Chem. 265 (16), 9153-9158 (1990)
 PUBMED [2160960](#)
 REMARK NUCLEOTIDE SEQUENCE.
 STRAIN=Type A / 62A
 REFERENCE 3 (residues 1 to 1296)
 AUTHORS East,A.K., Bhandari,M., Stacey,J.M., Campbell,K.D. and Collins,M.D.
 TITLE Organization and phylogenetic interrelationships of genes encoding

components of the botulinum toxin complex in proteolytic
Clostridium botulinum types A, B, and F: evidence of chimeric
sequences in the gene encoding the nontoxic nonhemagglutinin
component

JOURNAL Int. J. Syst. Bacteriol. 46 (4), 1105-1112 (1996)
PUBMED [8863443](#)
REMARK NUCLEOTIDE SEQUENCE OF 1-65.
STRAIN=Type A / 62A

REFERENCE 4 (residues 1 to 1296)
AUTHORS Betley,M.J., Somers,E. and DasGupta,B.R.
TITLE Characterization of botulinum type A neurotoxin gene: delineation
of the N-terminal encoding region

JOURNAL Biochem. Biophys. Res. Commun. 162 (3), 1388-1395 (1989)
PUBMED [2669749](#)
REMARK NUCLEOTIDE SEQUENCE OF 1-34.
STRAIN=Type A / Hall

REFERENCE 5 (residues 1 to 1296)
AUTHORS Fujita,R., Fujinaga,Y., Inoue,K., Nakajima,H., Kumon,H. and
Oguma,K.
TITLE Molecular characterization of two forms of
nontoxic-nonhemagglutinin components of Clostridium botulinum type
A progenitor toxins

JOURNAL FEBS Lett. 376 (1-2), 41-44 (1995)
PUBMED [8521962](#)
REMARK NUCLEOTIDE SEQUENCE OF 1-18.
STRAIN=Type A / NIH

REFERENCE 6 (residues 1 to 1296)
AUTHORS Schmidt,J.J., Sathyamoorthy,V. and DasGupta,B.R.
TITLE Partial amino acid sequence of the heavy and light chains of
botulinum neurotoxin type A

JOURNAL Biochem. Biophys. Res. Commun. 119 (3), 900-904 (1984)
PUBMED [6370252](#)
REMARK PROTEIN SEQUENCE OF 1-16.

REFERENCE 7 (residues 1 to 1296)
AUTHORS Dasgupta,B.R., Foley,J. and Niece,R.
TITLE Partial sequence of the light chain of botulinum neurotoxin type A

JOURNAL Biochemistry 26, 4162-4162 (1987)
REMARK PROTEIN SEQUENCE OF 1-46.

REFERENCE 8 (residues 1 to 1296)
AUTHORS DasGupta,B.R. and Dekleva,M.L.
TITLE Botulinum neurotoxin type A: sequence of amino acids at the
N-terminus and around the nicking site

JOURNAL Biochimie 72 (9), 661-664 (1990)
PUBMED [2126206](#)
REMARK PROTEIN SEQUENCE OF 1-5 AND 444-456.

REFERENCE 9 (residues 1 to 1296)
AUTHORS Sathyamoorthy,V., Dasgupta,B.R., Foley,J. and Niece,R.L.
TITLE Botulinum neurotoxin type A: cleavage of the heavy chain into two
halves and their partial sequences

JOURNAL Arch. Biochem. Biophys. 266 (1), 142-151 (1988)
PUBMED [3178218](#)
REMARK PROTEIN SEQUENCE OF 448-464 AND 872-895.

REFERENCE 10 (residues 1 to 1296)
AUTHORS Shone,C.C., Hambleton,P. and Melling,J.
TITLE Inactivation of Clostridium botulinum type A neurotoxin by trypsin
and purification of two tryptic fragments. Proteolytic action near
the COOH-terminus of the heavy subunit destroys toxin-binding
activity

JOURNAL Eur. J. Biochem. 151 (1), 75-82 (1985)
PUBMED [3896784](#)

REMARK PROTEIN SEQUENCE OF 448-482.

REFERENCE 11 (residues 1 to 1296)

AUTHORS Gimenez,J.A. and DasGupta,B.R.

TITLE Botulinum type A neurotoxin digested with pepsin yields 132, 97, 72, 45, 42, and 18 kD fragments

JOURNAL J. Protein Chem. 12 (3), 351-363 (1993)

PUBMED [8397793](#)

REMARK PROTEIN SEQUENCE OF 866-879 AND 1147-1218.

REFERENCE 12 (residues 1 to 1296)

AUTHORS Schiavo,G., Santucci,A., Dasgupta,B.R., Mehta,P.P., Jontes,J., Benfenati,F., Wilson,M.C. and Montecucco,C.

TITLE Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct COOH-terminal peptide bonds

JOURNAL FEBS Lett. 335 (1), 99-103 (1993)

PUBMED [8243676](#)

REMARK IDENTIFICATION OF SUBSTRATE.

REFERENCE 13 (residues 1 to 1296)

AUTHORS Binz,T., Blasi,J., Yamasaki,S., Baumeister,A., Link,E., Sudhof,T.C., Jahn,R. and Niemann,H.

TITLE Proteolysis of SNAP-25 by types E and A botulinal neurotoxins

JOURNAL J. Biol. Chem. 269 (3), 1617-1620 (1994)

PUBMED [8294407](#)

REMARK IDENTIFICATION OF SUBSTRATE.

REFERENCE 14 (residues 1 to 1296)

AUTHORS Rigoni,M., Caccin,P., Johnson,E.A., Montecucco,C. and Rossetto,O.

TITLE Site-directed mutagenesis identifies active-site residues of the light chain of botulinum neurotoxin type A

JOURNAL Biochem. Biophys. Res. Commun. 288 (5), 1231-1237 (2001)

PUBMED [11700044](#)

REMARK MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.

REFERENCE 15 (residues 1 to 1296)

AUTHORS Lacy,D.B., Tepp,W., Cohen,A.C., DasGupta,B.R. and Stevens,R.C.

TITLE Crystal structure of botulinum neurotoxin type A and implications for toxicity

JOURNAL Nat. Struct. Biol. 5 (10), 898-902 (1998)

PUBMED [9783750](#)

REMARK X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).

COMMENT On or before Mar 15, 2005 this sequence version replaced [gi:279630](#), [gi:115193](#), [gi:115174](#).

[FUNCTION] Inhibits acetylcholine release. The botulinum toxin binds with high affinity to peripheral neuronal presynaptic membrane, is then internalized by receptor-mediated endocytosis. The C-terminus of the heavy chain (H) is responsible for the adherence of the toxin to the cell surface while the N-terminus mediates transport of the light chain from the endocytic vesicle to the cytosol. After translocation, the light chain (L) hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking neurotransmitter release. Inhibition of acetylcholine release results in flaccid paralysis, with frequent heart or respiratory failure.

[CATALYTIC ACTIVITY] Limited hydrolysis of proteins of the neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No detected action on small molecule substrates.

[COFACTOR] Binds 1 zinc ion per subunit.

[SUBUNIT] Disulfide-linked heterodimer of a light chain (L) and a heavy chain (H).

[SUBCELLULAR LOCATION] Secreted.

[PHARMACEUTICAL] Available under the name BOTOX (Allergan) for the treatment of strabismus and blepharospasm associated with dystonia and cervical dystonia. Also used for the treatment of hemifacial

spasm and a number of other neurological disorders characterized by abnormal muscle contraction.

[MISCELLANEOUS] There are seven antigenically distinct forms of botulinum neurotoxin: Types A, B, C1, D, E, F, and G.

[SIMILARITY] Belongs to the peptidase M27 family.

[DATABASE] NAME=BOTOX product information Web site;

WWW='<http://www.botox.com/site/>'.

[DATABASE] NAME=Protein Spotlight; NOTE=Issue 19 of February 2002;

WWW='http://www.expasy.org/spotlight/back_issues/sptlt019.shtml'.

FEATURES	Location/Qualifiers
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<u>gene</u>	1..1296 /gene="botA" /note="synonyms: atx, bna"
<u>Protein</u>	1..1296 /gene="botA" /product="Botulinum neurotoxin type A precursor" /EC_number="3.4.24.69"
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<u>Region</u>	19..23 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
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	/evidence=experimental

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Region      604..617
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             /region_name="Helical region"
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Region      618..619
             /gene="botA"
             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      622
             /gene="botA"
             /region_name="Beta-strand region"
             /evidence=experimental
Region      625..626
             /gene="botA"
             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      627..647
             /gene="botA"
             /region_name="Transmembrane region"
             /note="Potential."
             /evidence=not_experimental
Region      628..629
             /gene="botA"
             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      633
             /gene="botA"
             /region_name="Beta-strand region"
             /evidence=experimental
Region      635..637
             /gene="botA"
             /region_name="Helical region"
             /evidence=experimental
Region      638..644
             /gene="botA"
             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      652..659
             /gene="botA"
             /region_name="Helical region"
             /evidence=experimental
Region      656..676
             /gene="botA"
             /region_name="Transmembrane region"
             /note="Potential."
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Region      661..664
             /gene="botA"
             /region_name="Helical region"
             /evidence=experimental
Region      679..681
             /gene="botA"
             /region_name="Beta-strand region"
             /evidence=experimental
Region      685..686
             /gene="botA"
             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      688..720
             /gene="botA"

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/region_name="Helical region"
/evidence=experimental
Region 721
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 722..742
/gene="botA"
/region_name="Helical region"
/evidence=experimental
Region 743..745
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 746..751
/gene="botA"
/region_name="Helical region"
/evidence=experimental
Region 752..753
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 758..759
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 766..799
/gene="botA"
/region_name="Helical region"
/evidence=experimental
Region 800
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 801..824
/gene="botA"
/region_name="Helical region"
/evidence=experimental
Region 825..829
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 831..833
/gene="botA"
/region_name="Helical region"
/evidence=experimental
Region 834..835
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 836..844
/gene="botA"
/region_name="Helical region"
/evidence=experimental
Region 845..846
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 853..855
/gene="botA"

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/region_name="Helical region"
/evidence=experimental
Region 860..871
/gene="botA"
/region_name="Helical region"
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Region 873..876
/gene="botA"
/region_name="Helical region"
/evidence=experimental
Region 876
/gene="botA"
/region_name="Conflict"
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Region 879..884

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/gene="botA"
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Region 885..886
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/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 887..890
/gene="botA"
/region_name="Beta-strand region"
/evidence=experimental
Region 891..892
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 892
/gene="botA"
/region_name="Conflict"
/note="S -> K (in Ref. 8)."
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Region 895..900

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Region 905..906
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/region_name="Beta-strand region"
/evidence=experimental
Region 911..912
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 913..917
/gene="botA"
/region_name="Beta-strand region"
/evidence=experimental
Region 920..921
/gene="botA"
/region_name="Hydrogen bonded turn"
/evidence=experimental
Region 924..928
/gene="botA"
/region_name="Beta-strand region"
/evidence=experimental
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Region      931..932
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             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      935..938
             /gene="botA"
             /region_name="Helical region"
             /evidence=experimental
Region      941..948
             /gene="botA"
             /region_name="Beta-strand region"
             /evidence=experimental
Region      956..959
             /gene="botA"
             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      961..966
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             /region_name="Beta-strand region"
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Region      975..979
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             /region_name="Beta-strand region"
             /evidence=experimental
Region      982..988
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             /region_name="Beta-strand region"
             /evidence=experimental
Region      990..991
             /gene="botA"
             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      994..1000
             /gene="botA"
             /region_name="Beta-strand region"
             /evidence=experimental
Region      1011..1012
             /gene="botA"
             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      1014..1021
             /gene="botA"
             /region_name="Beta-strand region"
             /evidence=experimental
Region      1023..1024
             /gene="botA"
             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      1026..1031
             /gene="botA"
             /region_name="Beta-strand region"
             /evidence=experimental
Region      1032..1033
             /gene="botA"
             /region_name="Hydrogen bonded turn"
             /evidence=experimental
Region      1034..1040
             /gene="botA"
             /region_name="Beta-strand region"
             /evidence=experimental

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Region      1042..1043
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               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1052..1058
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1063..1064
               /gene="botA"
               /region_name="Hydrogen bonded turn"
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Region      1066..1075
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1081..1090
               /gene="botA"
               /region_name="Helical region"
               /evidence=experimental
Region      1091..1092
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1094..1095
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1096
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1098
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1100..1101
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1104
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1106
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1111..1113
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1119..1120
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1122..1125
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental

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<u>Region</u>	1130..1131 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1134..1137 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1142 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1152 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1159..1163 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1173 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1175 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1176..1177 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1179..1186 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1187..1188 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1189..1195 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1197..1198 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1207..1209 /gene="botA" /region_name="Beta-strand region" /evidence=experimental
<u>Region</u>	1211..1213 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental
<u>Region</u>	1215..1216 /gene="botA" /region_name="Hydrogen bonded turn" /evidence=experimental

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Region      1218
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Region      1218
               /gene="botA"
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               /note="S -> Y (in Ref. 11). "
               /evidence=experimental
Region      1221..1223
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               /region_name="Beta-strand region"
               /evidence=experimental
Region      1226
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1228..1229
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1232
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Bond        bond(1235,1280)
               /gene="botA"
               /bond_type="disulfide"
               /evidence=experimental
Region      1235
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1237..1239
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1242..1243
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1248..1253
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1260..1264
               /gene="botA"
               /region_name="Beta-strand region"
               /evidence=experimental
Region      1265..1270
               /gene="botA"
               /region_name="Helical region"
               /evidence=experimental
Region      1271..1272
               /gene="botA"
               /region_name="Hydrogen bonded turn"
               /evidence=experimental
Region      1279..1280
               /gene="botA"
               /region_name="Hydrogen bonded turn"

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      /evidence=experimental
Region 1281
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      /region_name="Beta-strand region"
      /evidence=experimental
Region 1284..1285
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      /region_name="Beta-strand region"
      /evidence=experimental
Region 1289..1290
      /gene="botA"
      /region_name="Hydrogen bonded turn"
      /evidence=experimental
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ORIGIN

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121 stidtelkvi dtncinviqp dgsyrseeln lviigpsadi iqfecksfgh evlnltrngy
181 gstqyirfsp dftfgfeesl evdtnpllga gkfatdpavt lahelihagh rlygiaainp
241 rvfkvntnay yemsglevsf eelrtfgghd akfidslgen efrlyyyynkf kdiastlnka
301 ksivgttasl qymknvfkek yllsedtskg fsvdklkfdk lykmlteiyt ednfvkffkv
361 lnrktylnfd kavfkinivp kvnytiydgf nlrntnlaan fngqnteinn mnftklknft
421 glfefykllc vrgiitsktk sldkgynkal ndlcikvnnw dlffspsedn ftndlnkgee
481 itsdtnieaa eenisldliq qyyltnfnfdn epenisienl ssdiigqlel mpnierfpng
541 kkyeldkytm fhylraqefe hgksrialtn svneallnps rvytffssdy vkkvnkatea
601 amflgwveql vydfdetse vsttdkiadi tiiipyigpa lnignmlykd dfvgalifsg
661 avillefipe iaipvlgtfa lvsyiankv tvqtidnals krnekwddevy kyivtnwlak
721 vntqidlirk kmkealenqa eatkaiinyq ynqyteeeekn ninfniddls sklnessinka
781 mininkflnq csvsylvmsm ipygvkrled fdaslkdall kyidnrgtl igqvdrldkdk
841 vnntlstidp fqlskyvdnq rllstfteyi kniintsiln lryesnhlid lsryaskini
901 gskvnfdpid knqiqlfnle sskievilkn aivynsmyen fstsfwirip kyfnsislnn
961 eytiinmen nsgwkvslny geiiwtlqdt qeikqrvvfk ysqminisdy inrwifvtit
1021 nnrlnnskiy ingrlidqkp isnlgnihas nnimfkldgc rdthryiwik yfnlfdkeln
1081 ekeikdlydn qsnsgilkdf wgdylqydkp yymlnlydpn kyvdvnnvgi rgymylkgpr
1141 gsvmttniyl nsslyrgtkf iikkyasgnk dnivrndrv yinvvknke yrlatnasqa
1201 gvekilsale ipdvgnlsqv vvmkskndqg itnkckmnlq dnngndigfi gfhqfnniak
1261 lvasnwynrq ierssrtlgc swefipvddg wgerpl
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